

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 27, 2001, 16:55:40 ; Search time 45.66 Seconds
(without alignments)
749.622 Million cell updates/sec

Title: US-09-830-647-2

Perfect score: 1206
Sequence: 1 MNSGAMRIHSKHFQGGIOV.....LKKPFVKEEDMSQSPAVHLM 234

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP:REMBL_17:*
2: SP:archaea:*
3: SP:fungi:*
4: SP:human:*
5: SP_invertebrate:*
6: SP:mammal:*
7: SP:mhc:*
8: SP:organelle:*
9: SP:phage:*
10: SP:plant:*
11: SP:rodent:*
12: SP:virus:*
13: SP:vertebrate:*
14: SP:unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1206	100.0	234	4 Q9Y2M6	Q9Y2M6 homo sapien
2	1170	97.0	674	4 Q9UBU7	Q9UBU7 homo sapien
3	1077	89.3	676	11 Q99M00	Q99M00 cricetulus
4	974	80.8	321	11 Q9CXF2	Q9CXF2 mus musculus
5	974	80.8	663	11 Q9QZ41	Q9QZ41 mus musculus
6	784	65.0	601	4 Q75226	Q75226 homo sapien
7	208	17.2	170	4 Q9H912	Q9H912 homo sapien
8	170.5	14.1	1695	5 Q909R5	Q909R5 dirosophila
9	170.5	14.1	1695	5 Q9NK53	Q9NK53 dirosophila
10	170.5	14.1	1711	5 Q9VJL0	Q9VJL0 dirosophila
11	170.5	14.1	1711	5 Q9U9R4	Q9U9R4 dirosophila
12	114.5	9.5	647	3 Q93843	Q93843 emeticeila
13	101.5	8.4	779	10 Q81287	Q81287 arabidopsis
14	101	8.4	957	2 Q9AHL1	Q9AHL1 borrellia bu
15	99	8.2	849	2 Q9AHK4	Q9AHK4 borrellia bu
16	98	8.1	1173	2 Q9AHK6	Q9AHK6 borrellia bu
17	97	8.0	667	2 Q9Y117	Q9Y117 dirosophila
18	97	8.0	917	6 Q9TUB5	Q9TUB5 sus scrofa
19	95	7.9	1065	2 Q9AHK8	Q9AHK8 borrellia bu

20	94.5	7.8	667	2 Q9KK28	Q9KK28 streptococc
21	94.5	7.8	1438	2 Q99UK8	Q99UK8 stephylococ
22	92	7.6	1065	2 Q9AHK9	Q9AHK9 borrellia bu
23	91.5	7.6	681	2 Q9KK13	Q9KK13 streptococc
24	90	7.5	219	2 Q9ZLV6	Q9ZLV6 hellicobacte
25	89.5	7.4	616	13 Q9W721	Q9W721 brachydanio
26	89.5	7.4	1065	2 Q9AHK7	Q9AHK7 borrellia bu
27	89	7.4	509	5 Q15712	Q15712 paramecium
28	89	7.4	528	5 Q9YON2	Q9YON2 dirosophila
29	89	7.4	710	8 Q35064	Q35064 marchantia
30	89	7.4	871	10 Q9LYE6	Q9LYE6 arabidopsis
31	89	7.4	1119	2 Q51228	Q51228 borrellia bu
32	89	7.4	2091	5 Q9YU69	Q9YU69 dirosophila
33	88.5	7.3	657	2 Q9KK29	Q9KK29 streptococc
34	88.5	7.3	680	2 Q9KK11	Q9KK11 streptococc
35	88	7.3	805	4 Q95692	Q95692 homo sapien
36	87.5	7.3	392	2 Q50873	Q50873 borrellia bu
37	87.5	7.3	506	5 Q18822	Q18822 caenorhabdi
38	87.5	7.3	520	2 Q84054	Q84054 chlamydia t
39	87.5	7.3	715	10 Q9LNT9	Q9LNT9 arabidopsis
40	87	7.2	426	2 Q9KUL5	Q9KUL5 vibrio chol
41	87	7.2	1503	5 Q9V6P4	Q9V6P4 dirosophila
42	86.5	7.2	690	5 Q18413	Q18413 caenorhabdi
43	86.5	7.2	869	2 Q9KK27	Q9KK27 streptococc
44	86.5	7.2	887	11 Q88763	Q88763 rattus norv
45	86.5	7.2	1274	5 Q60985	Q60985 dictyostell

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	234 AA.
Q9Y2M6	Q9Y2M6	PRELIMINARY;	PRT;	234 AA.
AC	Q9Y2M6			
DT	01-NOV-1999 (TREMBLrel. 12, Created)			
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	ACTIVATOR OF S PHASE KINASE.			
GN	ASK/ H37			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Kumagai H., Sato N., Yamada M., Mahony D., Seghezzi W., Lees E.,			
RA	Arai K., Masai H.;			
RT	"A Novel Growth- and Cell Cycle-Regulated Protein, ASK, Activates			
RT	Human Cdc7-Related Kinase and is Essential for G1/S transition in			
RT	Mammalian Cells."			
RL	Mol. Cell. Biol. 0:0-0(1999).			
DR	EMBL; AB028070; BAA78327.1; -			
DR	InterPro; IPR001357; BRCT.			
DR	SMART; SM00292; BRCT. 1.			
SQ	SEQUENCE 234 AA; 26124 MW; 5035789FCF8472BC CRC64;			
Query Match	100.0%; Score 1206; DB 4; Length 234;			
Best Local Similarity	100.0%; Pred. No. 7.6e-92;			
Matches 234; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 MNSGAMRIHSKHFQGGIOVKNKKNRPSLSKLTDRNRPESKCKPLMGVFLDLPSTV 60			
DB	1 MNSGAMRIHSKHFQGGIOVKNKKNRPSLSKLTDRNRPESKCKPLMGVFLDLPSTV 60			
QY	61 SEKLQDIDKDLGGRVEPFLSKDISYLSNKKKPKQTIGRISPVSPSAYTAETTS 120			
DB	61 SEKLQDIDKDLGGRVEPFLSKDISYLSNKKKPKQTIGRISPVSPSAYTAETTS 120			
QY	121 PSKDGSSPKSPDVCVLSRGLVEKAIKDHDFPSSNLSNLSWGVKILHIDIRYIE 180			
DB	121 PSKDGSSPKSPDVCVLSRGLVEKAIKDHDFPSSNLSNLSWGVKILHIDIRYIE 180			

QY	181	ORKKELYLLKKSSTVYRDGKRVGSGAOKTRTGRLKKPKPVYKVEDMSGSPAVHLM	234
Db	181	ORKKELYLLKKSSTVYRDGKRVGSGAOKTRTGRLKKPKPVYKVEDMSGSPAVHLM	234
RESULT	2		
Q9UBU7		PRELIMINARY; PRT; 674 AA.	
AC	Q9UBU7		
DT	01-MAY-2000	(TREMBLrel. 13, Created)	
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)	
DT	01-JUN-2001	(TREMBLrel. 17, Last annotation update)	
DE	ACTIVATOR OF S PHASE KINASE.		
GN	ASK/H37 OR DBF4.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
OX	NCBI_Taxid:9606;		
RA	11		
RA	SEQUENCE FROM N.A.		
RA	Kumagai H., Sato N., Yamada M., Mahony D., Seghezzi W., Lees E.,		
RA	Arai K., Masai H.,		
RA	Y. Novel Related- and Cell Cycle-Regulated Protein, ASK, Activates		
RT	Human Cdc7-Related Kinase and Is Essential for G1/S Transition in		
RL	Mammalian Cells.";		
RL	Mol. Cell. Biol. 0:0-0(1999).		
RP	121		
RP	SEQUENCE FROM N.A.		
RP	Jiang W., Hunter T.;		
RT	"Mammalian Cdc7/Dbp1 Protein Kinase Complex Is Essential for		
RT	Initiation of DNA Replication.";		
RL	Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.		
RL	131		
RP	SEQUENCE FROM N.A.		
RT	Hollingsworth R.;		
RT	"Use of a semi-automated yeast two-hybrid system to identify proteins		
RL	that interact with the human Cdc7 protein.";		
RL	Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.		
DR	EMBL; A028069; BAA8326.1; -		
DR	EMBL; AF160249; AAD4191.1; -		
DR	EMBL; AF160876; AAD5357.1; -		
DR	Interpro: IPR001357 BRCt.		
DR	SMART: SM00292; BRCt; 1		
SO	SEQUENCE 674 AA; 76857 MW; 353FEB7E8507E5C CRC64;		
Query Match	97.08; Score 1170; DB 4; Length 674;		
Best Local Similarity	100.0%; Fred. No. 2.7e-88;		
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	MNSGAMRHISKGFQGIQVKNENKRPISLKTIDNRPKSKCKPILMGVYFLDIPSTI	60
Db	1	MNSGAMRHISKGFQGGIQVKNENKRPISLKTIDNRPKSKCKPILMGVYFLDIPSTI	60
QY	61	SEKLQDIDKDLGRVEEFLSKDIIYLSLNKKKKAQAQILGRTSPSPSAYTATTSPI	120
Db	61	SEKLQKIDKDLGRVEEFLSKDIYLSLNKKKKAQAQILGRTSPSPSAYTATTSPI	120
QY	121	PSHDGSEFSPTVCLSKGLLVEKAIKDHDIPNSITLSNALSMGVKILHDDIRYIE	180
Db	121	PSHDGSEFSPTVCLSKGLLVEKAIKDHDIPNSITLSNALSMGVKILHDDIRYIE	180
QY	181	QKKKELYLLKKSSTSVRDGKRVGSGAOKTRTGRLKKPKPVYKVEDMSQ	227
Db	181	QKKKELYLLKKSSTSVRDGKRVGSGAOKTRTGRLKKPKPVYKVEDMSQ	227
RESULT	3		
Q99MU0		PRELIMINARY; PRT; 676 AA.	
AC	Q99MU0		
DT	01-JUN-2001	(TREMBLrel. 17, Created)	

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DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE DBFA/ASK.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Cricetinae;
OC Cricetulus.
OC NCBI_TaxId=10029;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21147935; PubMed=11250080;
RA Guo H., Lee H.;
RT "Cloning and characterization of Chinese hamster homologous of yeast
RT DBFA (CDBFA4).";
RL Gene 264:249-256(2001).
DR EMBL: AF2924400; AAK21856.1;
SQ SEQUENCE 676 AA; 75849 MW; EC7EEDBD80D40B8C CRC64;

Query Match 89.3%; Score 1077; DB 11; Length 676;
Best Local Similarity 89.9%; Pred. No. 1,3e-80;
Matches 205; Conservative 13; Mismatches 10; Indels 0; Gaps

Oy 1 MSGCARHSHKGHGGIOVKNKRNKRPISLKTNTNPERKCKPMLMGVFFYLDLPSTYI 60
Db 1 MSGCARHSHKSHFGGIOVKNKRNPSLSLKTNTNPERKCKPMLMEKFFYLDLPSTYI 60
Oy 61 SEKLQMDIKDGGARVEEFLSKNDISYLSNKKKAKPAQFLGRIISFVSPESAATYETSPH 120
Db 1 SEKLQMDIKDGGARVEEFLSKNDISYLSNKKKAKPAQFLGVSFVSPESAATYETSPH 120
Oy 61 PSMDGSSFPSPPTVCLNSGKTLVEKRIKDHDFPNSNLSIALSMGKILHIDDIRYYIE 180
Db 1 PSMDGSSFPSPDRCVCLNSGKTLAEKAKVCHDFIPANSILSNALMGWKILHIDDIRYYIE 180
Oy 121 PSMDGSSFPSPPTVCLNSGKTLVEKRIKDHDFPNSNLSIALSMGKILHIDDIRYYIE 180
Db 121 PSMDGSSFPSPDRCVCLNSGKTLAEKAKVCHDFIPANSILSNALMGWKILHIDDIRYYIE 180
Oy 181 OKKKELYLTKSSTSVRQCGKRGVSGSGKQRTFRGRIKRPFFVVEEDMSQS 228
Db 181 OKKKECLSLKNSSTSVRQSGKAGTTOYKARTRGRIKRPFLKVEDVNRS 228

RESULT 4
OSGKXF2 PRELIMINARY; PRT: 321 AA.
AC O9GXF2
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE 14 DAYS EMBRYO LIVER cDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
DE CLONE:4432409802, FULL INSERT SEQUENCE.
OS Mus musculus (Mouse).
OC Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Muridae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX SFRATN=C57BL/6J; TISSUE=EMBRYONIC LIVER;
RA Kamei J., Shinozawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Katsuka T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aikawa K., Izawa A., Nishik K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Sakata T., Okazaki Y., Goshobori T., Bono H., Kasukawa T., Saito R.,
RA Saito K., Matsuda H., Asoburner M., Batalov S., Casavant T.,
RA Fietzschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirra L.M., Staudt P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido I., Furuno M., Kono H., Balderelli R., Barsch G.,
RA Brownstein M.J., Bult C., Plancher C., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hoffman M., Hume D.A., Kanlaya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima M., Mazzarelli J., Monnaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Suzuki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K., Welter C., Whitaker C., Wilming L.,

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RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection.",
 RL Nature 409:685-690(2001).
 DR EMBL: AK014480; BAB29383.1;
 SQ SEQUENCE 321 AA; 36324 MW; 741B172C952A4579 CRC64;

Query Match 80.8%; Score 974; DB 11; Length 321;
 Best Local Similarity 82.4%; Pred. No. 1.5e-72;
 Matches 187; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

OY 1 MNSGAMRIHSKHPGQIOVKNKRNPSLSKTDNRPEKSKCPKPMKVFYLDPSVTI 60
 DB 1 MNLFTMRHSKAPLPFGQIDNRKRNPSLSKADNRLEKSKYKPLMGKIFLDPSITI 60
 OY 61 SEKLOKIDKJGGRVEEPLSKDISYFVSNKKEAKYAQTIGRVSPPSPESAVTAETTSFH 120
 DB 61 CEKLOKIDKJGGRVEEPLSKDISYFVSNKKEAKYAQTIGRVSPPSPESAVTAETTSFH 120
 OY 121 PSHDSSFRSPDVTCLSGKILVEKAIKDHDPISNSILSNLSGKVLHIDDIRYIE 180
 DB 121 PSHDSSFRSPDVTCLSGKILVEKAIKDHDPISNSILSNLSGKVLHIDDIRYIE 180
 OY 181 OKKKELYLKKSSTSVRDGKRVSGAOKTRTGRLKPFVKVEDMSQ 227
 DB 181 OKKKELYLKKSSTSVRDGKRVSGAOKTRTGRLKPFVKVEDMSQ 227

RESULT 5
 ID 090241 PRELIMINARY; PRT; 663 AA.

AC 090241:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE DBF4-RELATED PROTEIN.
 GN ASK OR MUDBF4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99444905; PubMed-10517317;
 RA Lepke M., Pueltner V., Staib C., Kneissl M., Berger C., Hoehn K.,
 RA Nanda I., Schmid M., Grummt F.,
 RT "Identification, characterization and chromosomal localization of the
 RT cognate human and murine DBF4 genes.",
 RL Mol. Gen. Genet. 262:220-229(1999).
 DR EMBL: AJ003132; CAB56847.1; -.
 DR MSG: MGI:1351328; Ask.
 SQ SEQUENCE 663 AA; 74175 MW; 72E05CB87C3B1650 CRC64;

Query Match 80.8%; Score 974; DB 11; Length 663;
 Best Local Similarity 82.4%; Pred. No. 3.9e-72;
 Matches 187; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

OY 1 MNSGAMRIHSKHPGQIOVKNKRNPSLSKTDNRPEKSKCPKPMKVFYLDPSVTI 60
 DB 1 MNLFTMRHSKAPLPFGQIDNRKRNPSLSKADNRLEKSKYKPLMGKIFLDPSITI 60
 OY 61 SEKLOKIDKJGGRVEEPLSKDISYFVSNKKEAKYAQTIGRVSPPSPESAVTAETTSFH 120
 DB 61 CEKLOKIDKJGGRVEEPLSKDISYFVSNKKEAKYAQTIGRVSPPSPESAVTAETTSFH 120
 OY 121 PSHDSSFRSPDVTCLSGKILVEKAIKDHDPISNSILSNLSGKVLHIDDIRYIE 180
 DB 121 PSHDSSFRSPDVTCLSGKILVEKAIKDHDPISNSILSNLSGKVLHIDDIRYIE 180
 OY 181 OKKKELYLKKSSTSVRDGKRVSGAOKTRTGRLKPFVKVEDMSQ 227
 DB 181 OKKKELYLKKSSTSVRDGKRVSGAOKTRTGRLKPFVKVEDMSQ 227

DB 181 OKKKELYLKKSSTSVRDGKRVSGAOKTRTGRLKPFVKVEDMSQ 227

RESULT 6
 ID 075226 PRELIMINARY; PRT; 601 AA.

AC 075226:
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE WUSGCIH_RG135C18.1 PROTEIN (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Kellen J. Burkhardt J.,
 RT "The sequence of Homo sapiens BAC clone RG135C18.",
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Waterson R.,
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC005164; AAC23786.1; -.
 FT NON TER
 SQ SEQUENCE 601 AA; 68666 MW; 7FC90B0234C1345F CRC64;

Query Match 65.0%; Score 784; DB 4; Length 601;
 Best Local Similarity 100.0%; Pred. No. 1.6e-56;
 Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 74 RVEEPLSKDISYFVSNKKEAKYAQTIGRVSPPSPESAVTAETTSFHSPHSDSSFRSPDT 133
 DB 1 RVEEPLSKDISYFVSNKKEAKYAQTIGRVSPPSPESAVTAETTSFHSPHSDSSFRSPDT 60
 OY 134 VCLSGKILVEKAIKDHDPISNSILSNLSGKVLHIDDIRYIEOKKKELYLKKS 193
 DB 61 VCLSGKILVEKAIKDHDPISNSILSNLSGKVLHIDDIRYIEOKKKELYLKKS 120
 OY 194 TSVRDGKRVSGAOKTRTGRLKPFVKVEDMSQ 227
 DB 121 TSVRDGKRVSGAOKTRTGRLKPFVKVEDMSQ 154

RESULT 7
 ID 09H912 PRELIMINARY; PRT; 170 AA.

AC 09H912:
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE CDNA FL13087 FIS, CLONE NT2RP3002099.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
 RA Tagatsuma M., Hosofiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
 RA Yamamoto S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
 RA Yamamoto Y., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
 RA Niomiya K., Iwayanagi T.,
 RT "NEBO human cDNA sequencing project.",
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK023149; BAB14431.1; -.
 SQ SEQUENCE 170 AA; 18392 MW; C93EE702A59B282E CRC64;

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Query Match      17.2%; Score 208; DB 4; Length 170;
Best Local Similarity 36.4%; Pred. No. 9,6e-10;
Matches 55; Conservative 22; Mismatches 44; Indels 30; Gaps 4;

OY 21 KNEKRPPLSLKLTNDNPEKSKCKPLMGKVFYLDLPSTISEKLOKXIKDGGVREPLIS 80
DB 35 KQKNSPGARK-----HPSGKFLYLDLPARKNQLFLGALIQDLGVIGFLS 82
OY 81 KQSYLISNKEAFQTLGRT-----SPVPSBSATYAETTSRPHSDSSFKSPDYTC 135
DB 83 KEVSTIVSRREVK-ASSCKSHRCGCPSPSESEVREVTISAMVDKSHPRKRPVDSVP 141
OY 136 LSRGKLVEKAIKDHDFIPSNLSLNSLWSG 166
DB 142 LSRGKELLQKAIK-----NQVSWG 160

RESULT 8
OY09UR5 PRELIMINARY; PRT: 1695 AA.
AC O9UR5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CHIFFON.
OR CHIF OR CHIFFON OR BG:DS09218.2 OR CG5813.
OC Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CANTON-S;
RT *The Drosophila chifon gene is required for chorion gene
RT amplification and is related to the yeast Dbf4 regulator of DNA
RT replication and cell cycle.
RL Development 126:0-0(1999).
DR EMBL; AF158178; A048779.1; -
DR Flybase; FBgn0000307; chif.
DR InterPro; IPR000637; AT_hook.
DR Pfam; PF02178; AT_hook.1.
DR SMART; SM00384; AT_hook.1.
SQ SEQUENCE 1695 AA; 188080 MW; 1409D8A1587C4B0 CRC64;

Query Match      14.1%; Score 170.5; DB 5; Length 1695;
Best Local Similarity 26.8%; Pred. No. 2,2e-05;
Matches 59; Conservative 42; Mismatches 78; Indels 41; Gaps 9;

OY 27 PSLKLTNDNPEKSKCKPLMGKVFYLDLPSTISEKLOKXIKDGGVREPLIS 86
DB 32 PRVKYIRSK-----RPLCHRFYLDLIDCHQIAKRLIESDIAKLGHLFEFLSDITHF 83
OY 87 ISNKEAFQTLGRTISRPSPESATYAETTSRPHSHGSSFK-----SPDYCLSRGL 141
DB 84 VTDKE-----VIGTSGTGTPTST-PGTPTSHYQONCSARKNOMOSADADILSRVR 137
OY 142 LVEKAIKDHDFIPSNLSLNSLWSGKILHIDIRYIEQKKEL--YLKKSSTSVRDC 199
DB 138 STVGVVNSGNTPTSLKRSYTLW-----QTYAQRFTKRIQTELOKYL-----E 182
OY 200 GRVSGAOKTRTG--RLKRPVKVEDMSQS--PAVHLM 234
DB 183 GRKEGCGSTSPHIIQKKOYKIVKIESVKNRYRPRYHLI 222

RESULT 9
OY09NK53 PRELIMINARY; PRT: 1695 AA.
AC 09NK53;
DT 01-OCT-2000 (TREMBLrel. 15, Created)

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DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE CHIF PROTEIN.
OR CHIF OR BG:DS09218.2 OR CG5813.
OC Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y, AND CN BM SP;
RX MEDLINE-99403001; PubMed-10471707;
RA Ashburner M., Mista S., Roote J., Lewis S.E., Blazej R., Davis T.,
RA Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
RA Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
RA Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,
RA Celniker S., Rubin G.M.;
RT *An exploration of the sequence of a 2.9-Mb region of the genome of
RT Drosophila melanogaster: the Adh region..";
RL Genetics 153:179-219(1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=Y, AND CN BM SP;
RA Buitenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
RA Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
RA Houston K.A., Hummasti S.R., Katta R., Kearney L., Kim E., Lee B.,
RA Lewis S., Li P., Lomocan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
RA Nixon K., Paclob J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
RA Sethi H., Smlr E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
RA Zieran L.L., Rubin G.M.;
RN [3]
RP SEQUENCE FROM N.A.
RC MEDLINE-20196006; PubMed-10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.E.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Brottier P.,
RA Borkova D., Botchan M.R., Bouck B., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Faurin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Jastolin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagham C.,
RA Jaiswal M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Krevitz S., Kuip D., Lal Z.,
RA Lasko P., Lei T., Levytsky A.A., Li J., Li Z., Liang X., Lin X.,
RA Liu X., Maitel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclob J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M.D., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodedge T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

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SQ SEQUENCE 1711 AA; 189250 MW; B7D0F95517C4B9A9 CRC64;
 Query Match 14.1%; Score 170.5; DB 5; Length 1711;
 Best Local Similarity 26.8%; Pred. No. 2.3e-05;
 Matches 59; Conservative 42; Mismatches 78; Indels 41; Gaps 9;
 QY 27 PSLKSLKTDNRPKSKCKPLMGKRYFLDPSVTISEKLOKIDLGGRVEELSKDISYL 86
 DB 32 PPKYKPKR-----RPCHRFKFLDIDCHLAKRLIESDPLGCHLEFLFSDITR 83
 QY 87 ISNKKKFAQTLGRISVPSPESAVTAETSPHPSHDSGSK-----SPDYCLSRGL 141
 DB 84 VYDKPE-----VIGTSGTGPST--PGPTSHYQNDGSAKRNQOSNADALSRVR 137
 QY 142 LVEKAIKDHDFPNSNLSNALSMGVKILHIDIRYIEOKKREL--YLLKSGTSVRDG 199
 DB 138 STVGAVNSGNSFTPTSLKRSYTIW-----QDYAQRFKRIQTELRKQYL-----E 182
 QY 200 GKVSGGAQKTRTG--RLKKPFVKVEDMSQS--PAVHLM 234
 DB 183 GKKEGGGTSASPHHQLKKQYKIESVKRNYRPRYHLI 222
 RESULT 12
 QY 093843 PRELIMINARY; PRT; 647 AA.
 ID 093843;
 AC 093843;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE G1/S REGULATOR.
 GN NIMO.
 OS Emericella nidulans (Aspergillus nidulans).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiiales; Trichocomaceae; Emericella.
 NCBI_TaxID=5072;
 RN 11;
 RP SEQUENCE FROM N.A.
 RC STRAIN=RI33;
 RA James S.W., Prasanna K.A., Seachert P.C., Gyax S.E., Matura R.A.,
 RA Bullock K.A.;
 RT "nmo gene of Aspergillus nidulans."
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF014812; AAD0151.1;
 DR PROSITE; P500058; DNA_MISMATCH_REPAIR.1; UNKNOWN.1.
 SQ SEQUENCE 647 AA; 72842 MW; A84A547CFB3D0EFL CRC64;
 Query Match 9.5%; Score 114.5; DB 3; Length 647;
 Best Local Similarity 18.8%; Pred. No. 0.27;
 Matches 50; Conservative 44; Mismatches 87; Indels 85; Gaps 9;
 QY 14 PGGIIOVKNENRPSLSKTDNRPKSKCKPLMGK-----VFYLDPSVTISEKL 64
 DB 102 FKKLLVAARDKEROPOKATQKQEPANISISOMORHRRKAPHFVFYFPAVDIVRSKC 161
 QY 65 OKDINDLGRVEELSKDISYLSNKKKFAQTLGRISVPSPESAVTAET-----TSP 119
 DB 162 SROVATLGRKREKFPFSLVTHVYTSR-----PIP-PEIDRRAQOTHTODTPTN 207
 QY 120 HPSHDSGSKSPD-----TVCLSRGLLVEKAIKDHDFPNSNLSNALSMGVK 169
 DB 208 ESAGGGAALQTVNAELEMHLAVCPKREQ-----SODVLRHAREMGKMI 253
 QY 170 LHIIDIRYIEOKKREL--YLLKSGTSVRDGGRVSGAOKTRTGR-----214
 DB 254 WAVEKLOHMI-ATINDLTLNGSGHSTRNN-----AAGSOTKSRGKDDLQVONLDELNGPS 308
 QY 215 -----LKKPFVKVEDMSQ 227
 DB 309 DRSHLSVLKDLVLPFKGPFIVYHDME 334

RESULT 13
 QY 081287 PRELIMINARY; PRT; 779 AA.
 ID 081287;
 AC 081287;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE T14P8.6 PROTEIN (A74G02460 PROTEIN).
 GN T14P8.6 OR A74G02460.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 NCBI_TaxID=3702;
 RN 11;
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA WASHU;
 RT Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN 12;
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Kallick J., Elliott G., Cloud J.;
 RT "The sequence of A. thaliana T14P8."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN 13;
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Waterston R.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 RN 14;
 RP SEQUENCE FROM N.A.
 RA Lamar B., Stoneking T., Stumpf J., Mewes H.W., Lemcke K.,
 RA Meyer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN 15;
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF069298; AAC19275.1;
 DR EMBL; AL161494; CAB80739.1;
 DR HSSP; P23367; 1BKX.
 DR InterPro; IPR002099; DNA_mis_repair.
 DR InterPro; IPR003594; HATPase-C.
 DR Pfam; PF02518; HATPase-C; 1.
 DR PROSITE; P500058; DNA_MISMATCH_REPAIR.1; UNKNOWN.1.
 SQ SEQUENCE 779 AA; 86431 MW; B866313991FFC691 CRC64;
 Query Match 8.4%; Score 101.5; DB 10; Length 779;
 Best Local Similarity 22.9%; Pred. No. 4.1;
 Matches 48; Conservative 35; Mismatches 66; Indels 61; Gaps 9;
 QY 23 EKNRPSLSKSLKTDNRP--EKSK-----CKPLMGK-----VFYLD-----LPSVTISE 62
 DB 392 EKENSLSREVEINDSPMKRFKFKACGTAKGGGSLVHDVTHLTKTPSKGLPOLNYTE 451
 QY 63 KLODKIDLGRVEELSKDISYLSNKKKFAQ-----TLGR-----ISPPSPES 110
 DB 452 KVTASDLDLSR-----SSFAOSTLNTFVYTMGRKKNENISTILSETP 493
 QY 111 AYTAETSPHPSHDSGSKSPDYCLSRGLLVEKAIKDHDFPS--NSLSNALSMGVK 168
 DB 494 VLRNQTSYVEKSKFEVRLASRLVGCOLDMDVVISKEDMTSPERDSELCNRISPCTQ 553
 QY 169 ILHID-----DIRYIEOKKREL 189
 DB 554 ADVNERHERVLCQFNLCFLIAKLERDLFIV 583
 RESULT 14

Q9AHL1
ID Q9AHL1 PRELIMINARY; PRT: 957 AA.
AC Q9AHL1;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE LMP1.
GN LMP1.
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RA Dunn J.J.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF305601; AAK18793.1;
SQ SEQUENCE 957 AA; 109700 MW; BE362F3EDCE7024 CRC64;

Query Match 8.4%; Score 101; DB 2; Length 957;
Best Local Similarity 22.0%; Pred. No. 5.8;
Matches 56; Conservative 47; Mismatches 101; Indels 50; Gaps 13;

QY 22 NEKNRPSLSKLTDRRPEKSKCKP---LMGKYF--YLDLPSTISEKLOKIDKLG---- 72
DB 249 NNNNTTSLKKTIPSNQKSELSPPSOTIIGKITRPRY---SYLIKELYEIIDDINTGRV 304
QY 73 ---GRVEEFLSKDIS-----YLISNKKKEAKFAO-----TLGRISPPPSPE 109
DB 305 TLGKNRLKELIKKGLSNKFQKYNELIENSKNKEASNLTLTKKDIEPNLINIPKDPYKK 364
QY 110 SAYTAETTSPPHSDG---SSEKSPDYVCLSRGKLVEKAID-HDFT---PSNSILSNA 162
DB 365 EIFQLDKEDKNQHPGDLKSKVHSIKPIDLENTKSR-QQAIKDNLNEFLKNNPNDQAASKT 423
QY 163 LSWGVKILHIDDIRYIEQ-KKKELYLLKKSSTSVRDG--KRVGSGAQKTRT 218
DB 424 LAQANKIOHLEDLKSQVHSIKPIDLENTKSRQQAIDKDLNEFLKNNPNDQAASKT 483
QY 219 FVKVEDMSQSPAVH 232
DB 484 IQYLEDLKS--VH 495

RESULT 15
Q9AHR4
ID Q9AHR4 PRELIMINARY; PRT: 849 AA.
AC Q9AHR4;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE LMP1.
GN LMP1.
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NA0;
RA Dunn J.J.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF305611; AAK18803.1;
SQ SEQUENCE 849 AA; 97432 MW; 095DCC4DEACD69DF CRC64;

Query Match 8.2%; Score 99; DB 2; Length 849;

Best Local Similarity 22.2%; Pred. No. 7.3;
Matches 52; Conservative 45; Mismatches 89; Indels 48; Gaps 12;

QY 22 NEKNRPSLSKLTDRRPEKSKCKP---LMGKYF--YLDLPSTISEKLOKIDKLG---- 72
DB 249 NNNNTTSLKKTIPSNQKSELSPPSOTIIGKITRPRY---SYLIKELYEIIDDINTGRV 304

QY 73 ---GRVEEFLSKDIS-----YLISNKKKEAKFAO-----TLGRISPPPSPE 109
DB 305 TLGKNRLKELIKKGLSNKFQKYNELIENSKNKEASNLTLTKKDIEPNLINIPKDPYKK 364
QY 110 SAYTAETTSPPHSDG---SSEKSPDYVCLSRGKLVEKAID-HDFT---PSNSILSNA 162
DB 365 EIFQLDKEDKNQHPGDLKSKVHSIKPIDLENTKSR-QQAIKDNLNEFLKNNPNDQAASKT 423
QY 163 LSWGVKILHIDDIRYIEQ-KKKELYLLKKSSTSVRDG--KRVGSGAQKTRT 212
DB 424 LAQANKIOHLEDLKSQVHSIKPIDLENTKSRQQAIDKDLNEFLKNNPNDQAASKT 477

Search completed: December 27, 2001, 16:55:42
Job time: 242 sec

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